

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
  
OM nucleic - nucleic search, using sw model  
  
Run on: February 20, 2006, 19:27:44 ; Search time 64 Seconds  
(without alignments)  
1610.915 Million cell updates/sec  
  
Title: US-09-615-571A-1\_COPY\_510\_567  
Perfect score: 58  
Sequence: 1 catgaagtcaccgctctgc.....tggcctctcgtcttgc 58  
  
Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0  
  
Searched: 1303057 seqs, 888780828 residues  
  
Word size : 0

Total number of hits satisfying chosen parameters: 2606114  
  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
  
Post-processing: Listing first 45 summaries  
  
Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PCUTUS\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					*							
Result No.	Score	Query Match	Length	DB ID	Description							
1	58	100.0	2318	3	US-09-426-072-1	Sequence 1, Appli						
2	19	32.8	35060	3	US-08-814-095-7	Sequence 7, Appli						
3	18	31.0	27	3	US-09-426-072-3	Sequence 3, Appli						
4	17	29.3	601	3	US-09-949-016-24377	Sequence 24377, A						
5	17	29.3	601	3	US-09-949-016-199548	Sequence 199548,						
6	17	29.3	601	3	US-09-949-002-2643	Sequence 2643, Ap						
7	17	29.3	601	3	US-09-949-002-2644	Sequence 2644, Ap						
8	17	29.3	601	3	US-09-949-002-2645	Sequence 2645, Ap						
9	17	29.3	601	3	US-09-949-002-9913	Sequence 9913, Ap						
10	17	29.3	601	3	US-09-949-002-9914	Sequence 9914, Ap						
11	17	29.3	601	3	US-09-949-002-9915	Sequence 9915, Ap						
12	17	29.3	1029	3	US-09-799-451-312	Sequence 312, App						
13	17	29.3	9316	3	US-09-949-016-16181	Sequence 16181, A						
14	17	29.3	54286	3	US-09-949-002-837	Sequence 837, App						
15	17	29.3	66955	3	US-09-949-002-642	Sequence 642, App						
16	17	29.3	373182	3	US-09-949-016-17371	Sequence 17371, A						
17	17	29.3	373694	3	US-09-949-016-12062	Sequence 12062, A						
18	17	29.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli						
19	17	29.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli						
20	16	27.6	30	3	US-09-033-333-17	Sequence 17, Appl						
21	16	27.6	30	3	US-09-033-428-18	Sequence 18, Appl						
22	16	27.6	30	3	US-09-033-556-40	Sequence 40, Appl						
23	16	27.6	30	3	US-09-614-495-17	Sequence 17, Appl						
24	16	27.6	30	3	US-09-898-883-18	Sequence 18, Appl						

25	16	27.6	30	3	US-09-814-292-38	Sequence 38, Appl
26	16	27.6	30	3	US-09-875-228-24	Sequence 24, Appl
27	16	27.6	480	6	PCT-US96-04648-1	Sequence 1, Appli
c 28	16	27.6	1280	2	US-08-027-986-3	Sequence 3, Appli
c 29	16	27.6	2540	2	US-08-027-986-4	Sequence 4, Appli
30	16	27.6	7845	3	US-09-949-016-14467	Sequence 14467, A
31	16	27.6	23632	3	US-09-949-016-16270	Sequence 16270, A
c 32	16	27.6	34427	3	US-09-111-911-5	Sequence 5, Appli
33	16	27.6	35937	3	US-09-782-378A-3	Sequence 3, Appli
34	16	27.6	42053	3	US-09-949-016-15924	Sequence 15924, A
c 35	16	27.6	118136	3	US-09-949-016-12439	Sequence 12439, A
36	15	25.9	259	3	US-09-270-767-4753	Sequence 4753, Ap
37	15	25.9	259	3	US-09-270-767-20035	Sequence 20035, A
c 38	15	25.9	483	3	US-09-252-991A-11472	Sequence 11472, A
39	15	25.9	601	3	US-09-949-016-26718	Sequence 26718, A
c 40	15	25.9	601	3	US-09-949-016-32732	Sequence 32732, A
c 41	15	25.9	601	3	US-09-949-016-51836	Sequence 51836, A
42	15	25.9	601	3	US-09-949-016-54005	Sequence 54005, A
43	15	25.9	601	3	US-09-949-016-54006	Sequence 54006, A
44	15	25.9	601	3	US-09-949-016-108639	Sequence 108639,
45	15	25.9	601	3	US-09-949-016-108640	Sequence 108640,

ALIGNMENTS

RESULT 1  
US-09-426-072-1  
; Sequence 1, Application US/09426072  
; Patent No. 6146869  
; GENERAL INFORMATION:  
; APPLICANT: Paul Harris  
; APPLICANT: Kimberly M. Brown  
; TITLE OF INVENTION: Polypeptides Having Phospholipase B  
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same  
; FILE REFERENCE: 5951.000-US  
; CURRENT APPLICATION NUMBER: US/09/426,072  
; CURRENT FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 2318  
; TYPE: DNA  
; ORGANISM: Aspergillus oryzae  
US-09-426-072-1

Query Match 100.0%; Score 58; DB 3; Length 2318;  
Best Local Similarity 100.0%; Pred. No. 4e-22;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCTCTTGGCCTCTCTCGGCTTGTCT 58  
|||||  
Db 510 CATGAAGTCCACCGCTCTGCTTACTGGTCTCGGCTCTTGGCCTCTCTCGGCTTGTCT 567

RESULT 2  
US-08-814-095-7/c  
; Sequence 7, Application US/08814095  
; Patent No. 6025183  
; GENERAL INFORMATION:  
; APPLICANT: Soreq, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KOHN & ASSOCIATES  
; STREET: 30500 No. 6025183thwestern Highway, Suite 410  
; CITY: Farmington Hills  
; STATE: Michigan  
; COUNTRY: U.S.  
; ZIP: 48334

```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Cosmid including ACHE
; DESCRIPTION: promotor, ACHE gene and ARS gene"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 7q22
; FEATURE:
; NAME/KEY: promotor
; LOCATION: 4089..22464
; OTHER INFORMATION: /function= "ACHE Promotor"
; OTHER INFORMATION: /standard_name= "ACHE Promotor"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 22465..22537
; OTHER INFORMATION: /function= "non-translated"
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: 24090..25177
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "(translation start:
; OTHER INFORMATION: 24110)"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 2
; FEATURE:
; NAME/KEY: exon
; LOCATION: 25524..26009
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 3
; FEATURE:
; NAME/KEY: exon
; LOCATION: 27005..27274
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 4
; FEATURE:
; NAME/KEY: exon
; LOCATION: 27255..28007
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 5
; FEATURE:
;
;
; NAME/KEY: terminator
; LOCATION: 27385..27387
; FEATURE:
; NAME/KEY: exon
; LOCATION: 28008..28129
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 6
; FEATURE:
; NAME/KEY: terminator
; LOCATION: 28129..28131
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (34528..34895)
; OTHER INFORMATION: /function= "arsenite resistance
; OTHER INFORMATION: gene"
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (34092..34358)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 2
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (33779..33963)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 3
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (33493..33591)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 4
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (33297..33408)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 5
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (32959..33094)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 6
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (32569..32628)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 7
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (32386..32468)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 8
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (31894..32080)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 9
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (31363..31534)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 10
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (31131..31284)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 11
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (30816..31011)
; OTHER INFORMATION: /gene= "AR"
```

```

; OTHER INFORMATION: /number= 12
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (30470..30626)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 13
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (30187..30274)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 14
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (29945..30073)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 15
; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (29664..29856)
; OTHER INFORMATION: /gene= "ARS"
; OTHER INFORMATION: /number= 16
US-08-814-095-7

```

```

Query Match 32.8%; Score 19; DB 3; Length 35060;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 27 GTCTCGGCCTCTTGGCCTC 45
Db 6964 GTCTCGGCCTCTTGGCCTC 6946

```

# RESULT 3

```

US-09-426-072-3
; Sequence 3, Application US/09426072
; Patent No. 6146869
; GENERAL INFORMATION:
; APPLICANT: Paul Harris
; APPLICANT: Kimberly M. Brown
; TITLE OF INVENTION: Polypeptides Having Phospholipase B
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5951.000-US
; CURRENT APPLICATION NUMBER: US/09/426,072
; CURRENT FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-426-072-3

```

```

Query Match 31.0%; Score 18; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 ATGAAGTCCACCGCTCTG 19
Db 10 ATGAAGTCCACCGCTCTG 27

```

# RESULT 4

```

US-09-949-016-24377
; Sequence 24377, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

```

```

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24377
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-24377

```

```

Query Match 29.3%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 33 GCCTCTTGGCCTCTCTC 49
Db 478 GCCTCTTGGCCTCTCTC 494

```

# RESULT 5

```

US-09-949-016-199548
; Sequence 199548, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 199548
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-199548

```

```

Query Match 29.3%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 33 GCCTCTTGGCCTCTCTC 49
Db 478 GCCTCTTGGCCTCTCTC 494

```

# RESULT 6

```

US-09-949-002-2643/c
; Sequence 2643, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2643

```

```

; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-2643

Query Match          29.3%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 GCCTCTCTCGGTCTTGC 57
Db 46 GCCTCTCTCGGTCTTGC 30

RESULT 7
US-09-949-002-2644/c
; Sequence 2644, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2644
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-2644

Query Match          29.3%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 GCCTCTCTCGGTCTTGC 57
Db 403 GCCTCTCTCGGTCTTGC 387

RESULT 8
US-09-949-002-2645/c
; Sequence 2645, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2645
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-2645

Query Match          29.3%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 GCCTCTCTCGGTCTTGC 57
Db 41 GCCTCTCTCGGTCTTGC 57
Db 403 GCCTCTCTCGGTCTTGC 387

RESULT 9
US-09-949-002-9913/c
; Sequence 9913, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9913
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-9913

Query Match          29.3%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 GCCTCTCTCGGTCTTGC 57
Db 46 GCCTCTCTCGGTCTTGC 30

RESULT 10
US-09-949-002-9914/c
; Sequence 9914, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9914
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-9914

Query Match          29.3%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 GCCTCTCTCGGTCTTGC 57
Db 403 GCCTCTCTCGGTCTTGC 387

RESULT 11
US-09-949-002-9915/c
; Sequence 9915, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
```

```

Db 578 GCCTCTCTCGGTCTTGC 562

RESULT 9
US-09-949-002-9913/c
; Sequence 9913, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9913
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-9913

Query Match          29.3%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 GCCTCTCTCGGTCTTGC 57
Db 46 GCCTCTCTCGGTCTTGC 30

RESULT 10
US-09-949-002-9914/c
; Sequence 9914, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9914
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-9914

Query Match          29.3%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 GCCTCTCTCGGTCTTGC 57
Db 403 GCCTCTCTCGGTCTTGC 387

RESULT 11
US-09-949-002-9915/c
; Sequence 9915, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
```

; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000790  
; CURRENT APPLICATION NUMBER: US/09/949,002  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/231,401  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 10823  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9915  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-002-9915

Query Match 29.3%; Score 17; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 GCCTCTCTCGGTCTTGC 57  
|||||  
Db 578 GCCTCTCTCGGTCTTGC 562

RESULT 12  
US-09-799-451-312  
; Sequence 312, Application US/09799451  
; Patent No. 6783969  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ma, Yungqing  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Reena  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 803  
; CURRENT APPLICATION NUMBER: US/09/799,451  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 312  
; LENGTH: 1029  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (139)..(804)  
US-09-799-451-312

Query Match 29.3%; Score 17; DB 3; Length 1029;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 CTCGGCCTCTTGGCCTC 45  
|||||  
Db 466 CTCGGCCTCTTGGCCTC 482

RESULT 13  
US-09-949-016-16181/c

; Sequence 16181, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16181  
; LENGTH: 9316  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-16181

Query Match 29.3%; Score 17; DB 3; Length 9316;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 CTCGGCCTCTTGGCCTC 45  
|||||  
Db 8808 CTCGGCCTCTTGGCCTC 8792

RESULT 14  
US-09-949-002-837  
; Sequence 837, Application US/09949002  
; Patent No. 6900016  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000790  
; CURRENT APPLICATION NUMBER: US/09/949,002  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/231,401  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 10823  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 837  
; LENGTH: 54286  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-002-837

Query Match 29.3%; Score 17; DB 3; Length 54286;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 GCCTCTCTCGGTCTTGC 57  
|||||  
Db 46214 GCCTCTCTCGGTCTTGC 46230

RESULT 15  
US-09-949-002-642  
; Sequence 642, Application US/09949002  
; Patent No. 6900016  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000790

```
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 66955
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-642

Query Match      29.3%; Score 17; DB 3; Length 66955;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      41 GCCTCTCTCGGCTTGC 57
      |||||||||||||||
Db      58755 GCCTCTCTCGGCTTGC 58771

Search completed: February 20, 2006, 19:50:20
Job time : 70 secs
```



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
  
OM protein - nucleic search, using frame\_plus\_p2n model  
  
Run on: February 20, 2006, 19:49:29 ; Search time 236 Seconds  
(without alignments)  
3494.867 Million cell updates/sec  
  
Title: US-09-615-571A-2  
Perfect score: 464  
Sequence: 1 MKSTALLTGLGLLASGLAS.....GTTLREDAPIALKTPHTFSV 464

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0  
  
Searched: 1303057 seqs, 888780828 residues  
  
Word size: 1  
  
Total number of hits satisfying chosen parameters: 2599977

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
  
Post-processing: Listing first 45 summaries  
  
Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US09615571/runat\_17022006\_164409\_26327/app\_query.fasta\_1  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=olig\_p2n.rn1 -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss05h  
-USER=US09615571 @CGN 1 1 193 @runat\_17022006\_164409\_26327 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Match	Length	ID	Description
1	266	57.3	2318	3	US-09-426-072-1
2	10	2.2	692	3	US-09-533-559-4754
3	9	1.9	2242	3	US-09-620-312D-15
4	8	1.7	215	3	US-09-513-999C-19903
C 5	8	1.7	411	3	US-09-252-991A-3621
C 6	8	1.7	423	3	US-09-252-991A-3714
C 7	8	1.7	441	3	US-09-252-991A-3175
C 8	8	1.7	447	3	US-09-252-991A-3088

9	8	1.7	504	3	US-09-621-976-13586	Sequence 13586, A
10	8	1.7	531	3	US-09-489-039A-2202	Sequence 2202, Ap
11	8	1.7	573	3	US-09-533-559-1768	Sequence 1768, Ap
12	8	1.7	601	3	US-09-949-016-23390	Sequence 23390, A
C 13	8	1.7	601	3	US-09-949-016-38746	Sequence 38746, A
14	8	1.7	601	3	US-09-949-016-79450	Sequence 79450, A
15	8	1.7	601	3	US-09-949-016-79451	Sequence 79451, A
C 16	8	1.7	601	3	US-09-949-016-143736	Sequence 143736, A
17	8	1.7	601	3	US-09-949-016-176575	Sequence 176575, A
18	8	1.7	753	3	US-09-252-991A-15657	Sequence 15657, A
19	8	1.7	993	3	US-09-252-991A-15615	Sequence 15615, A
C 20	8	1.7	1027	3	US-09-533-559-332	Sequence 332, App
C 21	8	1.7	1086	3	US-09-902-540-3495	Sequence 3495, Ap
C 22	8	1.7	1089	3	US-09-134-001C-1833	Sequence 1833, Ap
C 23	8	1.7	1110	3	US-09-902-540-2970	Sequence 2970, Ap
C 24	8	1.7	1119	3	US-09-252-991A-3800	Sequence 3800, Ap
C 25	8	1.7	1416	3	US-09-252-991A-15670	Sequence 15670, A
C 26	8	1.7	1521	3	US-09-252-991A-15579	Sequence 15579, A
C 27	8	1.7	1596	3	US-08-976-063E-33	Sequence 33, Appl
C 28	8	1.7	1617	3	US-09-252-991A-3842	Sequence 3842, Ap
C 29	8	1.7	1629	3	US-09-252-991A-2699	Sequence 2699, Ap
C 30	8	1.7	1629	3	US-09-252-991A-2986	Sequence 2986, Ap
C 31	8	1.7	1656	3	US-09-252-991A-3669	Sequence 3669, Ap
C 32	8	1.7	1725	3	US-09-252-991A-2884	Sequence 2884, Ap
C 33	8	1.7	1788	3	US-09-248-796A-12489	Sequence 12489, A
C 34	8	1.7	1869	3	US-09-252-991A-15737	Sequence 15737, A
C 35	8	1.7	1946	3	US-09-882-835-1	Sequence 1, Appli
C 36	8	1.7	2226	3	US-09-252-991A-12520	Sequence 12520, A
C 37	8	1.7	2682	2	US-08-791-887-1	Sequence 1, Appli
C 38	8	1.7	2682	3	US-10-146-084-1	Sequence 1261, Ap
C 39	8	1.7	2823	3	US-09-976-594-131	Sequence 131, App
C 40	8	1.7	3331	3	US-09-999-833A-458	Sequence 458, App
C 41	8	1.7	4040	3	US-10-020-445A-458	Sequence 458, App
C 42	8	1.7	4040	3	US-09-583-110-2006	Sequence 2006, Ap
C 43	8	1.7	4941	3	US-08-961-527-47	Sequence 47, Appl
C 44	8	1.7	4945	3	US-09-620-312D-240	Sequence 240, App
C 45	8	1.7	4953	3		

ALIGNMENTS

RESULT 1  
US-09-426-072-1  
; Sequence 1, Application US/09426072  
; Patent No. 6146869  
; GENERAL INFORMATION:  
; APPLICANT: Paul Harris  
; APPLICANT: Kimberly M. Brown  
; TITLE OF INVENTION: Polypeptides Having Phospholipase B  
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same  
; FILE REFERENCE: 5951.000-US  
; CURRENT APPLICATION NUMBER: US/09/426,072  
; CURRENT FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 2318  
; TYPE: DNA  
; ORGANISM: Aspergillus oryzae  
US-09-426-072-1

Alignment Scores:  
Pred. No.: 1.99e-264 Length: 2318  
Score: 266.00 Matches: 266  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 57.3% Indels: 0  
DB: 3 Gaps: 0

US-09-615-571A-2 (1-464) x US-09-426-072-1 (1-2318)

QY 199 ProThrasnProAsnArgLeuCysAlaLeuAlaGlyThrAlaAlaGlyHisGlyLysAsn 218  
|||||

Db 1248 CCTACCAACCCCAACCGCTTGTGGCTCTGGCAGGAACCGCTGCTGGGCATGGCAAGAT 1307

Qy 219 AspAspAspPheLeuAsnTyrGlyIleSerSerLysSerIlePheGluAlaAlaAsnGlu 238  
|||||

Db 1308 GACGATGACTTCTGAACTATGGTATCTCTAGCAAGTCCATCTTCGAGGCCGCCAACGAG 1367

Qy 239 LysGlyValSerTrpLeuAsnTyrAspGlyThrAsnGlyGluPheGluProAspSerLeu 258  
|||||

Db 1368 AAGGGCGTGTCTGGCTCAACTACGATGGCACCACCGAGAATTCGAACCGGATTCTCTC 1427

Qy 259 PhePheThrTyrValAsnGlnThrSerArgSerAsnValValProValGluAsnPhePhe 278  
|||||

Db 1428 TTCTTCACTACGTCAACCCAGACCTCCCGGTCCAACGTGGTGGCCGTTGAAAACTTCTTC 1487

Qy 279 GlnAspAlaTyrLeuGlyValLeuProLysPheSerTyrIleAsnProSerCysCysGly 298  
|||||

Db 1488 CAAGACGCTACCTCGGTGTCTCCCTAAATTCTCTTACATTAACCCCTCCTGCTGCGGC 1547

Qy 299 ThrAsnThrAsnSerMetHisProThrGlyAsnValSerTyrGlyGluValPheValLys 318  
|||||

Db 1548 ACCAACACCAACTCCATGCACCCACCGGTAAAGTCTCCTACGGTGAGGTCTTCGTCAAG 1607

Qy 319 GlnIleTyrAspAlaIleArgGlnGlyProGlnTrpAspLysThrLeuLeuPheIleThr 338  
|||||

Db 1608 CAGATCTATGATGCCATTCCGCCAGGCCCCTCAGTGGGACAAAGACCCTGTCTTTCATTACC 1667

Qy 339 TyrAspGluThrGlyGlyPheTyrAspHisValProProProLeuAlaValArgProAsp 358  
|||||

Db 1668 TACGACGAGACCGGTGGCTTCTACGACCATGTCCCTCCCTCCTCGCCGTCCGCCCGGAC 1727

Qy 359 AsnLeuThrTyrThrGluThrAlaLysAsnGlyGlnLysTyrThrLeuHisPheAspArg 378  
|||||

Db 1728 AACCTGACTACACTGAGACTGCGAAGAACGGTCAGAAATACACTCTTCACTTCGACCGT 1787

Qy 379 LeuGlyGlyArgMetProThrTrpValIleSerProTyrSerLysLysGlyTyrIleGlu 398  
|||||

Db 1788 CTGGTGGCGCATGCCGACCTGGGTATCTCCCTTACAGTAAGAAGGATACATCGAG 1847

Qy 399 GlnTyrGlyThrAspProValThrGlyLysProAlaProTyrSerAlaThrSerValLeu 418  
|||||

Db 1848 CAGTACGGAACGGATCCCGTCACGGGCAAGCCCGTCCCTACAGTGCTACCTCCGTCCTC 1907

Qy 419 LysThrLeuGlyTyrLeuTrpAspIleGluAspPheThrProArgValAlaHisSerPro 438  
|||||

Db 1908 AAGACTCTCGGATATCTCTGGGACATCGAGGACTTCACCCCTCGTGTGCCCCACTCTCCA 1967

Qy 439 SerPheAspHisLeuIleGlyThrThrLeuArgGluAspAlaProIleAlaLeuLysThr 458  
|||||

Db 1968 TCCTTCGATCACCTGATCGGCACGACTTTCGTGAGGATGCTCTCTATTGCTCTCAAGACT 2027

Qy 459 ProHisThrPheSerVal 464  
|||||

Db 2028 CCCCATACCTTTTCGGTA 2045

RESULT 2

US-09-533-559-4754  
; Sequence 4754, Application US/095333559  
; Patent No. 6902887  
; GENERAL INFORMATION:  
; APPLICANT: Randy M. Berka  
; APPLICANT: Michael W. Rey  
; APPLICANT: Jeffrey R. Shuster  
; APPLICANT: Sakari Kauppinen  
; APPLICANT: Ib Groth Clausen  
; APPLICANT: Peter Bjarke Olsen  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; FILE REFERENCE: 5849.200-US  
; CURRENT APPLICATION NUMBER: US/09/533,559  
; CURRENT FILING DATE: 2000-03-22  
; EARLIER APPLICATION NUMBER: 09/273,623  
; EARLIER FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 7860

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4754  
; LENGTH: 692  
; TYPE: DNA  
; ORGANISM: Aspergillus oryzae  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(692)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-533-559-4754

Alignment Scores: Length: 692  
Pred. No.: 0.904 Matches: 10  
Score: 10.00 Conservative: 0  
Percent Similarity: 100.0% Mismatches: 0  
Best Local Similarity: 100.0% Indels: 0  
Query Match: 2.2% Gaps: 0  
DB: 3

US-09-615-571A-2 (1-464) x US-09-533-559-4754 (1-692)

Qy 358 AspAsnLeuThrTyrThrGluThrAlaLys 367  
|||||

Db 191 GATAACCTGACGTATACCGAAACGGCCAAG 220

RESULT 3

US-09-620-312D-15  
; Sequence 15, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 15  
; LENGTH: 2242  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (156)..(1649)  
US-09-620-312D-15

Alignment Scores: Length: 2242  
Pred. No.: 29.2 Matches: 9  
Score: 9.00 Conservative: 0  
Percent Similarity: 100.0% Mismatches: 0  
Best Local Similarity: 100.0% Indels: 0  
Query Match: 1.9%



DB: 3 Gaps: 0

US-09-615-571A-2 (1-464) x US-09-620-312D-15 (1-2242)

QY 12 LeuLeuAlaSerLeuGlyLeuAlaSer 20  
DB 300 CTCTGGCCCTCTGGGACTTGGCTCT 326

RESULT 4

US-09-513-999C-19903

; Sequence 19903, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 19903

; LENGTH: 215

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 58

; OTHER INFORMATION: w=a or t

US-09-513-999C-19903

Alignment Scores:

Pred. No.: 35.1 Length: 215

Score: 8.00 Matches: 8

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 1.7% Indels: 0

DB: 3 Gaps: 0

US-09-615-571A-2 (1-464) x US-09-513-999C-19903 (1-215)

QY 69 GlyGlyValArgGlnGlyLeu 76  
DB 150 GCGGGGTCCGCCGCCAGGGTTG 173

RESULT 5

US-09-252-991A-3621/c

; Sequence 3621, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 3621

; LENGTH: 411

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-3621

Alignment Scores:

Pred. No.: 64.4 Length: 411

Score: 8.00 Matches: 8

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 1.7% Indels: 0

DB: 3 Gaps: 0

US-09-615-571A-2 (1-464) x US-09-252-991A-3621 (1-411)

QY 10 LeuGlyLeuAlaSerLeuGly 17  
DB 229 CTCGGCCTGCTGGCGAGTCTCGGC 206

RESULT 6

US-09-252-991A-3714/c

; Sequence 3714, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 3714

; LENGTH: 423

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-3714

Alignment Scores:

Pred. No.: 66.1 Length: 423

Score: 8.00 Matches: 8

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 1.7% Indels: 0

DB: 3 Gaps: 0

US-09-615-571A-2 (1-464) x US-09-252-991A-3714 (1-423)

QY 10 LeuGlyLeuAlaSerLeuGly 17  
DB 122 CTCGGCCTGCTGGCGAGTCTCGGC 99

RESULT 7

US-09-252-991A-3175/c

; Sequence 3175, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 3175

; LENGTH: 441

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-3175

Alignment Scores:

Pred. No.: 68.7 Length: 441

Score: 8.00 Matches: 8

Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 1.7% Indels: 0  
DB: 3 Gaps: 0

US-09-615-571A-2 (1-464) x US-09-252-991A-3175 (1-441)

Qy 12 LeuLeuAlaSerLeuGlyLeuAla 19  
|||||  
Db 226 CTGCTGGCCAGCCTCGGCCTGGCC 203

RESULT 8  
US-09-252-991A-3088/c  
; Sequence 3088, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 3088  
; LENGTH: 447  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-3088

Alignment Scores:  
Pred. No.: 69.6 Length: 447  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 1.7% Indels: 0  
DB: 3 Gaps: 0

US-09-615-571A-2 (1-464) x US-09-252-991A-3088 (1-447)

Qy 12 LeuLeuAlaSerLeuGlyLeuAla 19  
|||||  
Db 332 CTGCTGGCCAGCCTCGGCCTGGCC 309

RESULT 9  
US-09-621-976-13586  
; Sequence 13586, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 13586  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 176  
; OTHER INFORMATION: n=a, g, c or t  
US-09-621-976-13586

Alignment Scores:  
Pred. No.: 77.9 Length: 504

Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 1.7% Indels: 0  
DB: 3 Gaps: 0

US-09-615-571A-2 (1-464) x US-09-621-976-13586 (1-504)

Qy 11 GlyLeuLeuAlaSerLeuGlyLeu 18  
|||||  
Db 418 GGCCTGTTGGCTAGCCTGGGCCTC 441

RESULT 10  
US-09-489-039A-2202  
; Sequence 2202, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 2202  
; LENGTH: 531  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2202

Alignment Scores:  
Pred. No.: 81.8 Length: 531  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 1.7% Indels: 0  
DB: 3 Gaps: 0

US-09-615-571A-2 (1-464) x US-09-489-039A-2202 (1-531)

Qy 407 GlyLysProAlaProTyrSerAla 414  
|||||  
Db 165 GGAAAGCCTGCACCATATTCAGCA 188

RESULT 11  
US-09-533-559-1768  
; Sequence 1768, Application US/09533559  
; Patent No. 6902887  
; GENERAL INFORMATION:  
; APPLICANT: Randy M. Berka  
; APPLICANT: Michael W. Rey  
; APPLICANT: Jeffrey R. Shuster  
; APPLICANT: Sakari Kauppinen  
; APPLICANT: Ib Groth Clausen  
; APPLICANT: Peter Bjarke Olsen  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; FILE REFERENCE: 5849.200-US  
; CURRENT APPLICATION NUMBER: US/09/533,559  
; CURRENT FILING DATE: 2000-03-22  
; EARLIER APPLICATION NUMBER: 09/273,623  
; EARLIER FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 7860  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1768  
; LENGTH: 573  
; TYPE: DNA  
; ORGANISM: Fusarium venenatum  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(573)

```
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-1768

Alignment Scores:
Pred. No.:      87.8      Length:      573
Score:          8.00      Matches:      8
Percent Similarity: 100.0%  Conservative: 0
Best Local Similarity: 100.0%  Mismatches: 0
Query Match:    1.7%      Indels:      0
DB:             3         Gaps:          0

US-09-615-571A-2 (1-464) x US-09-533-559-1768 (1-573)

QY      411 ProTyrSerAlaThrSerValleu 418
      |||||
Db       1 CCCTACTCCGCCACAAAGCGTCCTC 24

RESULT 12
US-09-949-016-23390
; Sequence 23390, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23390
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-23390

Alignment Scores:
Pred. No.:      91.8      Length:      601
Score:          8.00      Matches:      8
Percent Similarity: 100.0%  Conservative: 0
Best Local Similarity: 100.0%  Mismatches: 0
Query Match:    1.7%      Indels:      0
DB:             3         Gaps:          0

US-09-615-571A-2 (1-464) x US-09-949-016-23390 (1-601)

QY      15 SerLeuGlyLeuAlaSerProVal 22
      |||||
Db       265 TCCCTGGGACTTGCTTCCCTGTG 288

RESULT 13
US-09-949-016-38746/c
; Sequence 38746, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38746
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38746/c
```

```
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38746
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38746

Alignment Scores:
Pred. No.:      91.8      Length:      601
Score:          8.00      Matches:      8
Percent Similarity: 100.0%  Conservative: 0
Best Local Similarity: 100.0%  Mismatches: 0
Query Match:    1.7%      Indels:      0
DB:             3         Gaps:          0

US-09-615-571A-2 (1-464) x US-09-949-016-38746 (1-601)

QY      10 LeuGlyLeuAlaSerLeuGly 17
      |||||
Db       128 CTGGGCCTCCTTGCTTCTCTGGGA 105

RESULT 14
US-09-949-016-79450
; Sequence 79450, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79450
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-79450

Alignment Scores:
Pred. No.:      91.8      Length:      601
Score:          8.00      Matches:      8
Percent Similarity: 100.0%  Conservative: 0
Best Local Similarity: 100.0%  Mismatches: 0
Query Match:    1.7%      Indels:      0
DB:             3         Gaps:          0

US-09-615-571A-2 (1-464) x US-09-949-016-79450 (1-601)

QY      8 ThrGlyLeuGlyLeuAlaSer 15
      |||||
Db       177 ACTGGTCTTGGAAGCTCTGGCCTCG 200

RESULT 15
US-09-949-016-79451
; Sequence 79451, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
```

```

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79451
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-79451

```

Alignment Scores:		
Pred. No.:	91.8	601
Score:	8.00	8
Percent Similarity:	100.0%	0
Best Local Similarity:	100.0%	0
Query Match:	1.7%	0
DB:	3	0
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-09-615-571A-2 (1-464) x US-09-949-016-79451 (1-601)

Qy 8 ThrGlyLeuGlyLeuLeuAlaSer 15  
157 ACTGGTCTTGGACTCCTGGCCCTCG 180

Search completed: February 20, 2006, 19:54:20  
Job time : 240 secs